

CRF Errors Corrected by the STIC System Branch

#15

Serial Number: 09/463,494A

CRF Processing Date: 3/15/02

Edited by: DC

Verified by: DC (STIC staff)

ENTERED

1652

TECH CENTER 1600/2900

MAR 21 2002

RECEIVED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

RAW SEQUENCE LISTING

DATE: 03/15/2002

PATENT APPLICATION: US/09/463,494A

TIME: 10:41:58

Input Set : N:\Crf3\03072002\I463494A.raw

Output Set: N:\CRF3\03152002\I463494A.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Reetz, Manfred; Zonta, Albin; Schimossek, Klaus;
 3 Liebeton, Klaus; Jager, Karl-Erich

4 (ii) TITLE OF INVENTION: A Process for the Preparation and
 5 Identification of Novel Hydrolases Having Improved
 6 Properties

7 (iii) NUMBER OF SEQUENCES: 21

8 (iv) CORRESPONDENCE ADDRESS:

9 (A) ADDRESSEE: Norris McLaughlin & Marcus

10 (B) STREET: 220 East 42nd Street, 30th Floor

11 (C) CITY: New York

12 (D) STATE: New York

13 (E) COUNTRY: USA

14 (F) ZIP: 10017

15 (v) COMPUTER READABLE FORM:

16 (A) MEDIUM TYPE: Floppy disk

17 (B) COMPUTER: IBM PC compatible

18 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

19 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

20 (vi) CURRENT APPLICATION DATA:

C--> 21 (A) APPLICATION NUMBER: US/09/463,494A

C--> 22 (B) FILING DATE: 25-Jul-2000

23 (C) CLASSIFICATION:

24 (vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: PCT/EP98/04612

26 (B) FILING DATE: 23-JUL-1998

27 (A) APPLICATION NUMBER: DE 197 31 990.4

28 (B) FILING DATE: 25-JUL-1997

29 (viii) ATTORNEY/AGENT INFORMATION:

30 (A) NAME: Briscoe, Kurt G.

31 (B) REGISTRATION NUMBER: 33141

32 (C) REFERENCE/DOCKET NUMBER: STUDIEN 268

33 (ix) TELECOMMUNICATION INFORMATION:

34 (A) TELEPHONE: (212) 808-0700

35 (B) TELEFAX: (212) 808-0844

36 (2) INFORMATION FOR SEQ ID NO: 1:

37 (i) SEQUENCE CHARACTERISTICS:

38 (A) LENGTH: 30 base pairs

39 (B) TYPE: nucleic acid

40 (C) STRANDEDNESS: unknown

41 (D) TOPOLOGY: linear

42 (ii) MOLECULE TYPE: other nucleic acid

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43      (A) DESCRIPTION: /desc = "synthetic DNA"
44      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
45      GCGCAATTAA CCCTCACTAA AGGGAACAAA                      30
47 (2) INFORMATION FOR SEQ ID NO: 2:
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 27 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: unknown
52          (D) TOPOLOGY: linear
53      (ii) MOLECULE TYPE: other nucleic acid
54          (A) DESCRIPTION: /desc = "synthetic DNA"
55      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
56      GCGTAATACG ACTCACTATA GGGCGAA                      27
58 (2) INFORMATION FOR SEQ ID NO: 3:
59      (i) SEQUENCE CHARACTERISTICS:
60          (A) LENGTH: 1049 base pairs
61          (B) TYPE: nucleic acid
62          (C) STRANDEDNESS: unknown
63          (D) TOPOLOGY: unknown
64      (ii) MOLECULE TYPE: DNA (genomic)
65      (ix) FEATURE:
66          (A) NAME/KEY: CDS
67          (B) LOCATION:85..1017
68      (ix) FEATURE:
69          (A) NAME/KEY: mat_peptide
70          (B) LOCATION:163..1017
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
72      GGATCCCCCG GTTCTCCCGG AAGGATTCCG GCGATGGCTG GCAGGACGCG CCCCTCGGCC      60
73      CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TAT CTG CTC CCC CTC      111
74      Met Lys Lys Lys Tyr Leu Leu Pro Leu
75      -26 -25 -20
76      GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG      159
77      Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
78      -15 -10 -5
79      GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC      207
80      Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
81      1 5 10 15
82      ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT      255
83      Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
84      20 25 30
85      CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC      303
86      Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
87      35 40 45
88      AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG      351
89      Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
90      50 55 60
91      GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC      399
92      Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
93      65 70 75

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Input Set : N:\Crif3\03072002\I463494A.raw

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94      GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT      447
95      Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
96      80                      85                      90                      95
97      CCC GAC CTG ATC GCT TCC GCC ATC AGC GTC GGC GCC CCG CAC AAG GGT      495
98      Pro Asp Leu Ile Ala Ser Ala Ile Ser Val Gly Ala Pro His Lys Gly
99      100                      105                      110
100     TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC      543
101     Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
102     115                      120                      125
103     GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC      591
104     Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
105     130                      135                      140
106     TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG      639
107     Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu
108     145                      150                      155
109     GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG      687
110     Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
111     160                      165                      170                      175
112     CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC      735
113     Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
114     180                      185                      190
115     GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC      783
116     Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
117     195                      200                      205
118     CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG      831
119     Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
120     210                      215                      220
121     AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG      879
122     Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
123     225                      230                      235
124     GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG      927
125     Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
126     240                      245                      250                      255
127     AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC      975
128     Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
129     260                      265                      270
130     GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG      1017
131     Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
132     275                      280                      285
133     TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC      1049
135 (2) INFORMATION FOR SEQ ID NO: 4:
136     (i) SEQUENCE CHARACTERISTICS:
137         (A) LENGTH: 311 amino acids
138         (B) TYPE: amino acid
139         (D) TOPOLOGY: linear
140     (ii) MOLECULE TYPE: protein
141     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
142     Met Lys Lys Lys Tyr Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
143     -26 -25                      -20                      -15

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Input Set : N:\Crf3\03072002\I463494A.raw

Output Set: N:\CRF3\03152002\I463494A.raw

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144 Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
145 -10 -5 1 5
146 Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
147 10 15 20
148 Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
149 25 30 35
150 Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu
151 40 45 50
152 Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
153 55 60 65 70
154 Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
155 75 80 85
156 Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
157 90 95 100
158 Ile Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
159 105 110 115
160 Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
161 120 125 130
162 Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr
163 135 140 145 150
164 Gly Thr Gln Asn Ser Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
165 155 160 165
166 Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
167 170 175 180
168 Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
169 185 190 195
170 Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
171 200 205 210
172 Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
173 215 220 225 230
174 Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
175 235 240 245
176 Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr
177 250 255 260
178 Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
179 265 270 275
180 Arg Leu Lys Asn Ala Ser Leu
181 280 285

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183 (2) INFORMATION FOR SEQ ID NO: 5:

184 (i) SEQUENCE CHARACTERISTICS:

185 (A) LENGTH: 1049 base pairs

186 (B) TYPE: nucleic acid

187 (C) STRANDEDNESS: unknown

188 (D) TOPOLOGY: unknown

189 (ii) MOLECULE TYPE: DNA (genomic)

190 (ix) FEATURE:

191 (A) NAME/KEY: CDS

192 (B) LOCATION: 85..1017

193 (ix) FEATURE:

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Input Set : N:\Crf3\03072002\I463494A.raw

Output Set: N:\CRF3\03152002\I463494A.raw

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194      (A) NAME/KEY: mat_peptide
195      (B) LOCATION:163..1017
196      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
197      GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC      60
198      CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC      111
199                      Met Lys Lys Lys Ser Leu Leu Pro Leu
200                      -26 -25                      -20
201      GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG      159
202      Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
203                      -15                      -10                      -5
204      GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC      207
205      Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
206      1                      5                      10                      15
207      ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT      255
208      Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
209                      20                      25                      30
210      CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC      303
211      Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
212                      35                      40                      45
213      AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG      351
214      Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
215      50                      55                      60
216      GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC      399
217      Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
218      65                      70                      75
219      GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT      447
220      Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
221      80                      85                      90                      95
222      CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT      495
223      Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly
224                      100                      105                      110
225      TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC      543
226      Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
227                      115                      120                      125
228      GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC      591
229      Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
230      130                      135                      140
231      TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG      639
232      Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu
233      145                      150                      155
234      GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG      687
235      Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
236      160                      165                      170                      175
237      CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC      735
238      Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
239                      180                      185                      190
240      GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC      783
241      Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
242                      195                      200                      205

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/463,494A

DATE: 03/15/2002

TIME: 10:41:59

Input Set : N:\Crf3\03072002\I463494A.raw

Output Set: N:\CRF3\03152002\I463494A.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]